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TECH CENTER 1600/2900



1645 age 1 of 6

1600

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/591,447D

DATE: 04/29/2002 TIME: 16:41:15

Input Set : A:\KCO1003textfile.txt

Output Set: N:\CRF3\04292002\I591447D.raw

**ENTERED** 

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3 <110> APPLICANT: Chatfield, Steven N
         Dougan, Gordon
 4
 5
         Sydenham, Mark
 7 <120> TITLE OF INVENTION: Vaccines Containing Attenuated Bacteria
 9 <130> FILE REFERENCE: KCO1003US
11 <140> CURRENT APPLICATION NUMBER: US 09/591,447D
12 <141> CURRENT FILING DATE: 2001-06-09
14 <150> PRIOR APPLICATION NUMBER: UK 9726233.1
                                                           MAY U 7 2002
TECH CENTER 1600/2900
15 <151> PRIOR FILING DATE: 1997-12-11
17 <160> NUMBER OF SEQ ID NOS: 4
19 <170> SOFTWARE: MS-DOS
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22 <211> LENGTH: 1287
23 <212> TYPE: DNA
24 <213> ORGANISM: Salmonella typhimurium
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30 gccccccagg tagtcgataa agtcgcagcc gtcgtcaata atggcgtcgt gctggaaagc
                                                                         120
                                                                         180
32 gacgttgatg gettaatgea atcagteaaa etcaaegegg gteaggeagg teageagett
                                                                         240
34 ccggacgacg ccacgctgcg tcaccagatc ctggaacgtt tgattatgga tcaaattatc
36 ctgcagatgg gtcagaagat gggggtgaag atcacggatg agcagttgga tcagccatca
                                                                         360
38 qccaacatcq ccaaacaaaa caatatqacq atqqatcaga tqcqcaqccq tctgqcttac
                                                                         420
40 gatgggctga actattcaac ctaccgtaac cagattcgta aagagatgat tatctctgaa
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42 gtgcgcaaca atgaggttcg tcgccgtatc accgttttgc cgcaagaagt tgacgcgctg
44 gcaaaacaga ttggcaccca aaacgatgcc agcaccgagc tgaacctgag ccatatcctg
                                                                         540
                                                                         600
46 attgctctgc cggaaaaccc aacctccgag caggttaacg acgcgcagcg ccaggcggaa
                                                                         660
48 agcattgttq aaqaagcgcg taacggcgca gatttcggca aactggcgat tacctactct
                                                                         720
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52 gggattttcg cccaggcgct gagcaccgcg aagaaaggcg acattgtcgg cccgattcgc
                                                                         780
                                                                         840
54 teeggegteg getteeacat tetgaaagta aatgaeetge geggteagag ceagagtate
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56 teegtgaceg aagtteaege tegteaeatt etgettaage egtegeegat eatgaaegat
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58 cagcaggege geetgaaget ggaagaaate geggetgaea ttaagagtgg taaaaccaee
60 tttgccgctg cggcgaaaga gtactctcag gacccgggct ccgctaacca gggcggtgat
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62 ttgggttggg ctacgccaga tattttcgac ccggcgttcc gcgacgcgct aacgaagctg
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64 cataaaggcc aaataagcgc gccggtacac tcctctttcg gctggcatct gatcgaattg
                                                                        1140
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66 ctggatacgc gtaaggtaga caaaaccgat gcggcgcaga aagatcgcgc ttatcgtatg
68 ctgatgaacc gtaaattctc agaagaagcg gcgacctgga tgcaagaaca gcgcgccact
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73 <210> SEQ ID NO: 2
74 <211> LENGTH: 427
75 <212> TYPE: PRT
76 <213> ORGANISM: Salmonella typhimurium
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78 <400> SEQUENCE: 2

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80 Met Lys Asn Trp Lys Thr Leu Leu Gly Ile Ala Met Ile Ala Asn 83 Thr Ser Phe Ala Ala Pro Gln Val Val Asp Lys Val Ala Ala Val Val 25 86 Asn Asn Gly Val Val Leu Glu Ser Asp Val Asp Gly Leu Met Gln Ser 89 Val Lys Leu Asn Ala Gly Gln Ala Gly Gln Gln Leu Pro Asp Asp Ala 92 Thr Leu Arg His Gln Ile Leu Glu Arg Leu Ile Met Asp Gln Ile Ile 75 70 95 Leu Gln Met Gly Gln Lys Met Gly Val Lys Ile Thr Asp Glu Gln Leu 90 85 98 Asp Gln Pro Ser Ala Asn Ile Ala Lys Gln Asn Asn Met Thr Met Asp 105 • 101 Gln Met Arg Ser Arg Leu Ala Tyr Asp Gly Leu Asn Tyr Ser Thr Tyr 120 115 104 Arg Asn Gln Ile Arg Lys Glu Met Ile Ile Ser Glu Val Arg Asn Asn 135 140 107 Glu Val Arg Arg Ile Thr Val Leu Pro Gln Glu Val Asp Ala Leu 155 150 110 Ala Lys Gln Ile Gly Thr Gln Asn Asp Ala Ser Thr Glu Leu Asn Leu 170 165 113 Ser His Ile Leu Ile Ala Leu Pro Glu Asn Pro Thr Ser Glu Gln Val 185 180 116 Asn Asp Ala Gln Arg Gln Ala Glu Ser Ile Val Glu Glu Ala Arg Asn 200 195 119 Gly Ala Asp Phe Gly Lys Leu Ala Ile Thr Tyr Ser Ala Asp Gln Gln 122 Ala Leu Lys Gly Gly Gln Met Gly Trp Gly Arg Ile Gln Glu Leu Pro 235 230 125 Gly Ile Phe Ala Gln Ala Leu Ser Thr Ala Lys Lys Gly Asp Ile Val 250 245 128 Gly Pro Ile Arg Ser Gly Val Gly Phe His Ile Leu Lys Val Asn Asp 265 131 Leu Arg Gly Gln Ser Gln Ser Ile Ser Val Thr Glu Val His Ala Arg 275 280 134 His Ile Leu Leu Lys Pro Ser Pro Ile Met Asn Asp Gln Gln Ala Arg 300 295 137 Leu Lys Leu Glu Glu Ile Ala Ala Asp Ile Lys Ser Gly Lys Thr Thr 315 310 140 Phe Ala Ala Ala Ala Lys Glu Tyr Ser Gln Asp Pro Gly Ser Ala Asn 330 325 143 Gln Gly Gly Asp Leu Gly Trp Ala Thr Pro Asp Ile Phe Asp Pro Ala 345 340 146 Phe Arg Asp Ala Leu Thr Lys Leu His Lys Gly Gln Ile Ser Ala Pro 355 360 149 Val His Ser Ser Phe Gly Trp His Leu Ile Glu Leu Leu Asp Thr Arg 370 375 152 Lys Val Asp Lys Thr Asp Ala Ala Gln Lys Asp Arg Ala Tyr Arg Met \_ \_

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Input Set : A:\KCO1003textfile.txt

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395
                        390
153 385
155 Leu Met Asn Arg Lys Phe Ser Glu Glu Ala Ala Thr Trp Met Gln Glu
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163 <211> LENGTH: 1287
164 <212> TYPE: DNA
165 <213> ORGANISM: Escherichia coli
167 <400> SEQUENCE: 3
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171 gccccccagg tagtcgataa agtcgcagcc gtcgtcaata acggcgtcgt gctggaaagc
                                                                          120
173 gacgttgatg gattaatgca gtcggtaaaa ctgaacgctg ctcaggcaag gcagcaactt
                                                                          180
175 cctgatgacg cgacgctgcg ccaccaaatc atggaacgtt tgatcatgga tcaaatcatt
                                                                          240
177 ctgcagatgg ggcagaaaat gggagtgaaa atctccgatg agcagctgga tcaggcgatt
                                                                          300
179 gctaacatcg cgaaacagaa caacatgacg ctggatcaga tgcgcagccg tctggcttac
                                                                          360
181 gatggactga actacaacac ctatcgtaac cagatccgca aagagatgat tatctctgaa
                                                                          420
183 gtgcgtaaca acgaggtgcg tcgtcgcatc accatcctgc cgcaggaagt cgaatccctg
                                                                          480
                                                                          540
185 gcgcagcagg tgggtaacca aaacgacgcc agcactgagc tgaacctgag ccacatcctg
                                                                          600
187 atcccgctgc cggaaaaccc gacctctgat caggtgaacg aagcggaaag ccaggcgcgc
                                                                          660
189 gccattgtcg atcaggcgcg taacggcgct gatttcggta agctggcgat tgctcattct
191 gccgaccagc aggcgctgaa cggcggccag atgggctggg gccgtattca ggagttgccc
                                                                          720
193 gggatcttcg cccaggcatt aagcaccgcg aagaaaggcg acattgttgg cccgattcgt
                                                                          780
195 tccggcgttg gcttccatat tctgaaagtt aacgacctgc gcggcgaaag caaaaatatc
                                                                          840
197 teggtgaceg aagtteatge tegecatatt etgetgaaac egtegeegat eatgactgae
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199 gaacaggccc gtgtgaaact ggaacagatt gctgctgata tcgagagtgg taaaacgact
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201 tttgctgccg caacgaaaga gttctctcag gatccagtct ctgctaacca gggcggcgat
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203 ctcggctggg ctacaccaga tattttcgat ccggccttcc gtgacgccct gactcgcctg
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205 aacaaaggtc aaatgagtgc accggttcac tetteatteg getggeattt aategaactg
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207 ctggataccc gtaatgtcga taaaaccgac gctgcgcaga aagatcgtgc ataccgcatg
                                                                         1200
209 ctgatgaacc gtaagttctc ggaagaagca gcaagctgga tgcaggaaca acgtgccagc
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214 <210> SEQ ID NO: 4
215 <211> LENGTH: 428
216 <212> TYPE: PRT
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225
                 20
227 Asn Asn Gly Val Val Leu Glu Ser Asp Val Asp Gly Leu Met Gln Ser
                                 40
            35
230 Val Lys Leu Asn Ala Ala Gln Ala Arg Gln Gln Leu Pro Asp Asp Ala
233 Thr Leu Arg His Gln Ile Met Glu Arg Leu Ile Met Asp Gln Ile Ile
                                             75
                         70
236 Leu Gln Met Gly Gln Lys Met Gly Val Lys Ile Ser Asp Glu Gln Leu
                                         90
237
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| 239<br>240 | Asp        | Gln        | Ala        | Ile<br>100 | Ala | Asn        | Ile        | Ala        | Lys<br>105 | Gln | Asn        | Asn        | Met        | Thr<br>110 | Leu        | Asp        |
|------------|------------|------------|------------|------------|-----|------------|------------|------------|------------|-----|------------|------------|------------|------------|------------|------------|
|            | Gln        | Met        | Arg<br>115 |            | Arg | Leu        | Ala        | Tyr<br>120 | Asp        | Gly | Leu        | Asn        | Tyr<br>125 | Asn        | Thr        | Tyr        |
| 245<br>246 | Arg        | Asn<br>130 | Gln        | Ile        | Arg | Lys        | Glu<br>135 | Met        | Ile        | Ile | Ser        | Glu<br>140 | Val        | Arg        | Asn        | Asn        |
| 248        | Glu<br>145 | Val        | Arg        | Arg        | Arg | Ile<br>150 | Thr        | Ile        | Leu        | Pro | Gln<br>155 | Glu        | Val        | Glu        | Ser        | Leu<br>160 |
| 252        |            |            |            |            | 165 |            |            |            |            | 170 |            |            |            |            | Asn<br>175 |            |
| 255        |            |            |            | 180        |     |            |            |            | 185        |     |            |            |            | 190        | Gln        |            |
| 258        |            |            | 195        |            |     |            |            | 200        |            |     |            |            | 205        |            | Arg        |            |
| 261        |            | 210        |            |            |     |            | 215        |            | ,          |     |            | 220        |            |            | Gln        |            |
| 264        | 225        |            |            |            |     | 230        |            |            |            |     | 235        |            |            |            | Leu        | 240        |
| 267        | _          |            |            |            | 245 |            |            |            |            | 250 |            |            |            |            | Ile<br>255 |            |
| 270        |            |            |            | 260        |     |            |            |            | 265        |     |            |            |            | 270        | Asn        |            |
| 273        |            |            | 275        |            |     |            |            | 280        |            |     |            |            | 285        |            | Ala        |            |
| 276        |            | 290        |            |            |     |            | 295        |            |            |     |            | 300        |            |            | Ala        |            |
| 279        | 305        |            |            |            |     | 310        |            |            |            |     | 315        |            |            |            | Thr        | 320        |
| 282        |            |            |            |            | 325 |            |            |            |            | 330 |            |            |            |            | Ala<br>335 |            |
| 285        |            |            |            | 340        |     |            |            |            | 345        |     |            |            |            | 350        | Pro        |            |
| 288        |            |            | 355        |            |     |            |            | 360        |            |     |            |            | 365        |            | Ala        |            |
| 291        |            | 370        |            |            |     |            | 375        |            |            |     |            | 380        |            |            | Thr        |            |
| 294        | 385        |            |            |            |     | 390        |            |            |            |     | 395        |            |            |            | Arg        | 400        |
| 297        |            |            |            |            | 405 |            |            |            |            | 410 |            |            | ттр        | met        | Gln<br>415 | GIU        |
| 299<br>300 | Gln        | Arg        | Ala        | Ser<br>420 | Ala | Tyr        | val        | ьуs        | Ile<br>425 | Leu | ser        | ASN        |            |            |            |            |

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/591,447D

DATE: 04/29/2002 TIME: 16:41:16

Input Set : A:\KCO1003textfile.txt

Output Set: N:\CRF3\04292002\I591447D.raw